

Nucleotide and Amino Acid Sequence of AIM-I

51	GGCACGAGCGGCTGCCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATG	8
16	CCGTGCTCGCCGACGGACCGACTGAATGTCGTAGTCTGAGACTGTCCAAGTACCGATAC	M A M 3
9	ATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTATTCACA	68
4	TACCTCCAGGTCCCCCTGGGTCGGACCCCTGTCGGACGACAGACTAGCACTAGAAGTGT	23
24	M E V Q G G P S L G Q T C V L I V I F T	
69	GTGCTCCTGCAGTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAG	128
24	CACGAGGACGTCAGAGAGACACCCGACATTGAATGCACATGAAATGGTTGCTCGACTTC	
129	V L L Q S L C V A V T Y V Y F T N E L K	43
44	CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTAAAGAAGATGACAGT	188
189	GTCTACGTCCTGTTCATGAGGTTTACCGTAACGAAACAAAGAATTTCTTACTGTCA	
64	Q M Q D K Y S K S G I A C F L K E D D S	63
189	TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCTGCTGGCAAGTCAGTGGCAA	248
64	ATAACCTGGGGTTACTGCTCTCTCATACTTGTGGGGACGACCGTTCAACCGTT	
249	Y W D P N D E E S M N S P C W Q V K W Q	83
84	CTCCGTCAGCTCGTTAGAAAGATGATTTGAGAACCTCTGAGGAAACCATTCTACAGTT	308
309	GAGGCAGTCGAGCAATCTTCTACTAAAACCTCTGGAGACTCCCTGGTAAAGATGTCAA	
104	L R Q L V R K M I L R T S E E T I S T V	103
369	CAAGAAAAGCAACAAATATTCTCCCTAGTGAGAGAAAGAGGTCTCAGAGAGTAGCA	368
124	GTTCTTTCTGTTGTTTATAAAGAGGGATCACTCTCTTCCAGGAGTCTCATCGT	
429	Q E K Q Q N I S P L V R E R G P Q R V A	123
144	CGTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTCTCCAAACTCCAAGAAT	428
124	CGAGTGTATTGACCCCTGGCTCCTCTTCGTTGTAAACAGAAGAGGTTGAGGTTCTTA	
429	A H I T G T R G R S N T L S S P N S K N	143
144	GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCAATT	
144	CTTTCCGAGACCCGGCGTTTATTTGAGGACCCCTAGTAGTTCTCACCCGTAAGTAAG	488
144	E K A L G R K I N S W E S S R S G H S F	163

FIG.1A

489	CTGAGCAACTTGCACTTGAGGAATGGTGAACGGTCATCCATGAAAAAGGGTTTACTAC	548
164	GACTCGTTAACGTGAACTCCTTACCACTTGACCAGTAGGTACTTTTCCAAAATGATG L S N L H L R N G E L V I H E K G F Y Y	183
549	ATCTATTCCAAACATACTTGCATTCAGGAGGAAATAAGAAAACACAAAGAACGAC	608
184	TAGATAAGGGTTGTATGAAAGCTAAAGTCCTCCTTATTTCTTTGTGTTCTTGCTG I Y S Q T Y F R F Q E E I K E N T K N D	203
609	AAACAAATGGTCCAATATATTACAAATACACAAGTTATCCTGACCTATATTGTTGATG	668
204	TTTGTGTTACCAAGGTTATATAATGTTATGTGTTCAATAGGACTGGGATATAACAACTAC K Q M V Q Y I Y K Y T S Y P D P I L L M	223
669	AAAAGTGCTAGAAATAGTTGTTGGCTAAAGATGCAGAATATGGACTCTATTCCATCTAT	728
224	TTTCACGATCTTATCAACAAACCAAGATTCTACGTCTTACCTGAGATAAGGTAGATA K S A R N S C W S K D A E Y G L Y S I Y	243
729	CAAGGGGAATATTGAGCTTAAAGGAAAATGACAGAATTGTTCTGTAACAAATGAG	788
244	GTTCCTTCTTATAAACTCGAATTCTTACTGTCTTAAACAAAGACATTGTTACTC Q G G I F E L K E N D R I F V S V T N E	263
789	CACTTGATAGACATGGACCATGAAGGCCAGTTTCTGGGGCTTTAGTTGGCTAACTG	848
264	GTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAATCAACCGATTGAC H L I D M D H E A S F F G A F L V G	281
849	ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGAATTCAGTTTCAAGGATGATAACTA	908
909	TGGACCTTCTTTCGTTATTGGAGTTCACTGATAAGTCCTACTATGTGAT TGAAGATGTTCAAAAAATCTGACCAAAACAAACAGAAAACAGAAAACAAAAAAAC	968
969	ACTTCTACAAAGTTTTAGACTGGTTTGTGTTGTCTTTGTCTTTGTTTGTGTTTG CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATTCTACAAACACACACTGTTCTG	1028
1029	GAGATACGTTAGACTCATCTCGTCGGTGTGGTTTAAAGATGTTGTGTGACAAGAC AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTCAGGACTCTACCT	1088
1089	TTTCACTGAGTGAATAGGGTTCTTACTTTAACGACTTTCTAGAAAGTCCTGAGATGG CATATCAGTTGCTAGCAGAAATCTAGAAGACTGTCAGCTCCAAACATTAATGCAATGG	1148
	GTATAGTCAAACGATCGTCTTAAAGATCTTCTGACAGTCGAAGGTTGTAATTACGTTACC	

FIG. 1B

FIG. 1C

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 % Identity = 22.892 %)

4 MEVQGGPSLGQTCVLIVIFTVL.....LQSLCVAVTYV 36
:: :...:...:...:... | : | .. .:...
15 vdssasspwappgtv1pcptsvprrrpgqrrppppppp1pppppppp1p 64

37 YFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQ 86
.. |...: ..|. |:| : . :.. . :|: .:|..
65 p1p..1p1kkrgnhstg1c11vm..ffmvlvalvg1g1gmfq1.fh1qk 109

87 LVRKMLRTSEETISTVQEKKQNIISPLVRERGPQRVAAHITGTRGRSNTL 136
: .: .||: . . . ||| . . . |: . | .||:| . |:|. .
110 elaelrestsqmhtasslekqighpsppkekkelrkvahlt...gksnsr 156

137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYIYS 186
| | ..:.. | :||. .: .:|||:||. |:||:|||
157 smplewedty.....giv11sgvkykkgg1vinetglyfrys 193

187 QTYFRFQEEIKENTKNDKQMVKYIYKYTS.YPDPILLMK\$ARNSCWSKDA 235
..||| . . . |: .: .:||. .| ||: .:||. . |: . .
194 kvyfr.....gqscnn1p1shkvymrnskypqd1vmmegkmmssycttgq 237

236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
:: | | |::|:|...|:::|. |.. |:::....||| : :
238 mwar.ssy1gavfn1tsadhlyvnvsels1vnfeesqtffg1ykl 281

FIG.2

Alignment Report of AIM-1, hFas Ligand, TNF- α and TNF- β by Clustal Method with PAM250 Residue Weight Table

	10	20	30	
1	MAMMEVQGGPSL-----GQT	CVLIVIFTVL		AIM 1
1	MQQPMNYPCPQIFWVDSSAT	SSWAPPGSVF		FAS LIGAND
1	M-----			tnfa.pep
1	M-----		TPPERLF	tnfb.pep
	40	50	60	
26	LQSLCVAVTYVYFTNELKQM	QDKYSKSGIA		AIM 1
31	PCPSCGPRG-----PDQR	RP PPPPPPVSPLP		FAS LIGAND
2	-----	STESMIRDVE		tnfa.pep
9	LPRVC CGTT-----			tnfb.pep
	70	80	90	
56	CFLKEDDSYWD	PNDDEESMN	SPCWQVKWQLR	AIM 1
57	--PPSQPLPLP	PLTPLKK	DHNTNLWLPVV	FAS LIGAND
12	--LAEEALP-----KK	TGGPQGSRRC	LWLL	tnfa.pep
17	-----	-----	-----	tnfb.pep
	100	110	120	
86	QLVRKMLR	TSEETISTVQ	KEKQQNISPLVR	AIM 1
85	FMVILVAL	VGMSG	LG-MYQLFHLQ	FAS LIGAND
32	FLSFLSFL	IVAGATT	LAEELR	tnfa.pep
21	LLGLLVL	LFCLL	HFGVIGPQRE	tnfb.pep
	130	140	150	
116	EKGQRVA	AHITGTRGR	SNLSSPNSKNEK	AIM 1
114	EFT-NQSL	KVSSFEKQIANP	STPSEKKEPR	FAS LIGAND
62	ESPRDL	SLISPLAQAVR	SSRTPSD-----K	tnfa.pep
34	GLP-GVGL	TPSAAQ	TARQHPKMHLAHSTLK	tnfb.pep
	160	170	180	
146	ALGRKINS	-----	WEISSRSGH	AIM 1
143	SVAHLTGNPH	HSRSIPL	PLEWEDTYGTALI	FAS LIGAND
88	PVAHV	VANPQAE	GQ-LQWLNR	tnfa.pep
63	PAAH	LIGDP	SKQNSLLWRA	tnfb.pep
			NTDRAFLQDC	

FIG. 3A

	190	200	210	
167	L H L R N G K L V I H E K G F Y Y I Y S Q T Y F R F Q E E I			AIM 1
172	V K Y K K G G L V I N E T G L Y F V Y S K V Y F R G Q S C N			FAS LIGAND
117	V E L R D N Q L V V P S E G L Y L I Y S Q V L F K G Q S C -			tnfa.pep
92	F S L S N N S L L V P T S G I Y F V Y S Q V V F S C K A Y S			tnfb.pep
	220	230	240	
197	K E N T K N D K Q M V Q Y I Y K Y T S - Y P D P I L L L M K S			AIM 1
202	N Q P - - - - - L N H K V Y M R N S K Y P E D L V L M E E			FAS LIGAND
146	- - - P S T H V L L T H T I S R I A V S Y Q T K V N L L S A			tnfa.pep
122	P K A P S S P L Y L A H E V Q L F S S Q Y P F H V P L L S S			tnfb.pep
	250	260	270	
226	A R N S C W S K D A E Y G L - - - - - Y S I Y Q G G I F E L			AIM 1
226	K R L N Y C - - - - - T T G Q I W A H S S Y L G A V F N L			FAS LIGAND
173	I K S P C Q R E T P E G A E A K P W Y E P I Y L G C V F Q L			tnfa.pep
152	Q K M V Y P - - - - - G L Q E P W L H S M Y H G A A F Q L			tnfb.pep
	280	290	300	
251	K E N D R I F V S V T N E H L I D K D H E A S - F F G A F L			AIM 1
250	T S A D H L Y V N I S Q L S L I N F E E S - K T F F G L Y -			FAS LIGAND
203	E K G D R L S A E I N R P D Y L D F A E S G Q V Y F G I I -			tnfa.pep
176	T Q G D Q L S T R T D G I P H L V L S P S - T V F F G A F -			tnfb.pep
280	V G -			AIM 1
278	- K L			FAS LIGAND
232	- A L			tnfa.pep
204	- A L			tnfb.pep

Decoration 'Decoration #1': Box residues that match the Consensus within 2 distance units.

FIG.3B

REGIONAL ANALYSIS OF AIM-1 PROTEIN

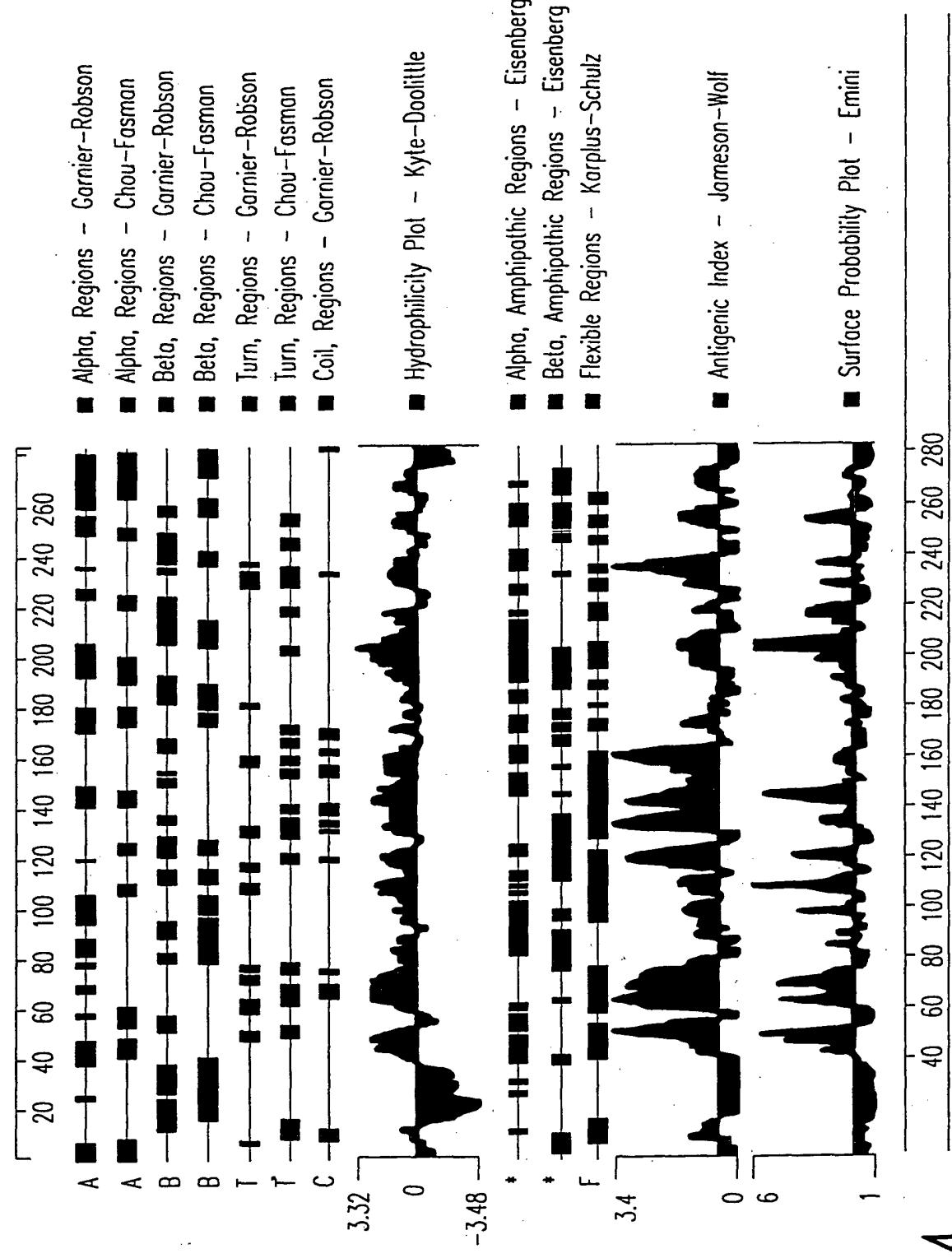


FIG. 4